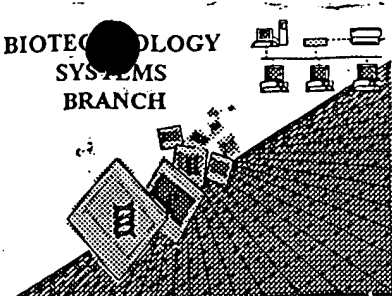


Re-run

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,140

Source: Per/09

Date Processed by STIC: 6/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/647,140

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

## RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

Does Not Comply  
Corrected Diskette Needed

P.6

```

3 <110> APPLICANT: Fox Chase Cancer Center
4      Kruh, Gary D.
5      Lee, Kun
6      Belinsky, Martin G.
7      Bain, Lisa J.
9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
10     Nucleic Acids and Methods of Use Thereof
12 <130> FILE REFERENCE: FCCC-98-02
14 <140> CURRENT APPLICATION NUMBER: 09/647,140
C--> 15 <141> CURRENT FILING DATE: 2001-05-21
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
18 <151> PRIOR FILING DATE: 1999-03-26
20 <150> PRIOR APPLICATION NUMBER: 60/079,759
21 <151> PRIOR FILING DATE: 1998-03-27
23 <150> PRIOR APPLICATION NUMBER: 60/095,153
24 <151> PRIOR FILING DATE: 1998-08-03
26 <160> NUMBER OF SEQ ID NOS: 18
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 4231
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
37  ggacaggcgt ggcggccgga gccccagcat ccctgcttga ggtccaggag cggagcccg 60
38  ggccaccgcc gcctgatcag cgcgaccccg gcccgcgccc gccccgcccg gcaagatgct 120
39  gcccggtgtac caggagggtga agcccaaccc gctgcaggac gcgaacatct gctcacgcgt 180
40  gttctttctg tggctcaatc ccttgtttaa aattggccat aaacggagat tagaggaaga 240
41  tgatatgtat tcagtgtctc cagaagaccg ctacacagcac cttggagagg agttgcaagg 300
42  gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt ctttaacaag 360
43  agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta cgtaattga 420
44  ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt attttgaaaa 480
45  ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca cgggtgtgac 540
46  tttttgcacg ctcatcttgg ctatactgca tcacttatat ttttatcacg ttcagtgtgc 600
47  tgggatgagg ttacgagtga ccatgtgcca tatgatttat cggaaggcac ttcgtcttag 660
48  taacatggcc atgggggaaga caaccacagg ccagatagtc aatctgctgt ccaatgatgt 720
49  gaacaagttt gatcagggtga cagtgttctt acacttcctg tgggcaggac cactgcaggc 780
50  gatcgacgtg actgccctac tctggatgga gataggaata tcgtgccttg ctgggatggc 840
51  agttctaatc attctcctgc ccttg:aaag ctgttttggg aagttgttct catcactgag 900
52  gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag ttataactgg 960
53  tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaatctta ttaccaattt 1020
54  gagaaagaag gagatttcca agattctgag aagttcctgc ctacagggga tgaatttggc 1080
55  ttcgtttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct acgtgctcct 1140
56  cggcagtggt atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg gggctgtgcg 1200
57  gctgacgggt accctcttct tccccctcag cattgagagg gtgtcagagg caatcgtcag 1260
58  catccgaaga atccagacct ttttgctact tgatgagata tcacagcgca accgtcagct 1320
59  gccgtcagat ggtaaaaaga tgggtcatgt gcaggatttt actgcttttt gggataaggc 1380
60  atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg aattgttagc 1440

```

## RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

61	tgtggtcggc	cccgtgggag	caggggaagtc	atcactgtta	agtgccgtgc	tcggggaatt	1500
62	ggccccaagt	cacgggctgg	tcagcgtgca	tggaagaatt	gcctatgtgt	ctcagcagcc	1560
63	ctgggtgttc	tcgggaactc	tgaggagtaa	tattttat	gggaagaaat	atgaaaagga	1620
64	acgatatgaa	aaagtcataa	aggcttgtgc	tctgaaaaag	gatttacagc	tggtggagga	1680
65	tggtgatctg	actgtgatag	gagatcgggg	aaccacgctg	agtggagggc	agaaagcacg	1740
66	ggtaaaccctt	gcaagagcag	tgtatcaaga	tgctgacatc	tatctcctgg	acgatcctct	1800
67	cagtgcagta	gatgcggaag	ttagcagaca	cttggtcgaa	ctgtgtattt	gtcaaatttt	1860
68	gcattgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaaag	ctgcaagtca	1920
69	gattctgata	ttgaaagatg	gtaaaatggg	gcagaagggg	acttacactg	agttcctaaa	1980
70	atctggtata	gattttggct	cccttttaaa	gaaggataat	gaggaaagtg	aacaacctcc	2040
71	agttccagga	actcccacac	taagggaatcg	taccttctca	gagtcttcgg	tttgggtctca	2100
72	acaatcttct	agaccctcct	tgaaagatgg	tgctctggag	agccaagata	cagagaatgt	2160
73	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttggttttc	aggcctataa	2220
74	gaattacttc	agagctgggtg	ctcactggat	tgtcttcatt	ttccttattc	tcctaaacac	2280
75	tgcagctcag	gttgccctatg	tgcttcaaga	ttgggtggctt	tcatactggg	caaacaaaca	2340
76	aagtatgcta	aatgtcactg	taaatggagg	aggaaatgta	accgagaagc	tagatcttaa	2400
77	ctggtactta	ggaattttatt	caggttttaac	tgtagctacc	gttctttttg	gcatagcaag	2460
78	atctctattg	gtattctacg	tccttggtta	ctcttcacaa	actttgcaca	acaaaatggt	2520
79	tgagtcaatt	ctgaaagctc	cgggtattatt	ctttgataga	aatccaatag	gaagaatttt	2580
80	aaatcgtttc	tccaaagaca	ttggacactt	ggatgatttg	ctgccgctga	cgtttttaga	2640
81	tttcatccag	acattgctac	aagtgggttg	tgtggtctct	gtggctgtgg	ccgtgattec	2700
82	ttggatcgca	atacccttgg	ttcccttgg	aatcattttc	atttttcttc	ggcgatattt	2760
83	tttgaaaacg	tcaagagatg	tgaagcgcct	ggaactctaca	actcggagtc	cagtgttttc	2820
84	ccacttgta	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaa	cagaagagag	2880
85	gtgtcaggaa	ctgtttgatg	cacaccagga	tttacattca	gaggcttggg	tcttgtttt	2940
86	gacaacgtcc	cgctggttcg	ccgtccgtct	ggatgccatc	tgtgccatgt	ttgtcatcat	3000
87	cgttgccttt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	ttggtttggc	3060
88	actgtcctat	gccctcacgc	tcattgggat	gtttcagtgg	tgtgttcgac	aaagtgtgta	3120
89	agttgagaat	atgatgatct	cagtagaaag	ggctattgaa	tacacagacc	ttgaaaaaga	3180
90	agcaccttgg	gaatatcaga	aacgcccacc	accagcctgg	ccccatgaag	gagtgataat	3240
91	ctttgacaat	gtgaacttca	tgtacagtc	aggtgggcct	ctggtactga	agcatctgac	3300
92	agcactcatt	aaatcacaa	aaaagggttg	cattgtggga	agaaccggag	ctggaaaaag	3360
93	ttccctcatc	tcagcccttt	ttagattgtc	agaaccggaa	ggtaaaattt	ggattgataa	3420
94	gatcttgaca	actgaaattg	gacttcacga	tttaaggga	aaaatgtcaa	tcataacctca	3480
95	ggaacctgtt	ttgttcaactg	gaacaatgag	gaaaaacctg	gatcccttta	aggagcacac	3540
96	ggatgaggaa	ctgtggaatg	ccttacaaga	ggtacaactt	aaagaaacca	ttgaagatct	3600
97	tcctggtaaa	atggatactg	aattagcaga	atcaggatcc	aatttttagtg	ttggacaaag	3660
98	acaactgggtg	tgcttggcca	gggcaattct	caggaaaaat	cagatattga	ttattgatga	3720
99	agcgacggca	aatgtggatc	caagaactga	tgagttaata	caaaaaaaaa	tccgggagaa	3780
100	atttgccac	tgaccgtgc	taaccattgc	acacagattg	aacaccatta	ttgacagcga	3840
101	caagataatg	gttttagatt	caggaagact	gaagaatat	gatgagccgt	atgttttgct	3900
102	gcaaaataaa	gagagcctat	tttacaagat	ggtgcaacaa	ctgggcaagg	cagaagccgc	3960
103	tgccctcact	gaaacagcaa	aacaggtata	cttcaaaaga	aattatccac	atattggtca	4020
104	cactgaccac	atggttacaa	acacttccaa	tggacagccc	tcgaccttaa	ctattttcga	4080
105	gacagcactg	tgaatccaac	caaatgtca	agtccgttcc	gaaggcattt	tccactagtt	4140
106	tttgactat	gtaaaccaca	ttgtactttt	ttttactttg	gcaacaaata	tttatacata	4200
107	caagatgcta	gttcatttga	atattttctcc	c			4231
110	<210> SEQ ID NO: 2						
111	<211> LENGTH: 1325						

## RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

```

112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
117 1 5 10 15
118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
119 20 25 30
120 Ile Gly His Lys Arg Arg Leu Glu Asp Asp Met Tyr Ser Val Leu
121 35 40 45
122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
123 50 55 60
124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
125 65 70 75 80
127 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
128 85 90 95
129 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
130 100 105 110
131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
132 115 120 125
133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
134 130 135 140
135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
136 145 150 155 160
137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
138 165 170 175
139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Gly
140 180 185 190
141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
142 195 200 205
143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
144 210 215 220
145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
146 225 230 235 240
147 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
148 245 250 255
149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
150 260 265 270
151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
152 275 280 285
153 Tyr Ala Thr Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
154 290 295 300
155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
156 305 310 315 320
157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
158 325 330 335
159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
160 340 345 350
161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
162 355 360 365

```

## RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

```

163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164      370      375      380
165 Arg Ile Gln Thr Phe Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166      385      390      395      400
167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168      405      410      415
169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170      420      425      430
171 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
172      435      440      445
173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174      450      455      460
175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176      465      470      475      480
177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178      485      490      495
179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180      500      505      510
181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182      515      520      525
183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184      530      535      540
185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186      545      550      555      560
187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188      565      570      575
190 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
191      580      585      590
192 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
193      595      600      605
194 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
195      610      615      620
196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197      625      630      635      640
198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199      645      650      655
200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201      660      665      670
202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203      675      680      685
204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205      690      695      700
206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207      705      710      715      720
208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
209      725      730      735
210 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
211      740      745      750
212 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr

```

DATE: 06/18/2001

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

213																	
214	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly	Ile	Ala	Arg	Ser	Leu	
215		770						775				780					
216	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln	Thr	Leu	His	Asn	Lys	
217	785					790					795					800	
218	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu	Phe	Phe	Asp	Arg	Asn	
219					805					810					815		
220	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	Asp	Ile	Gly	His	Leu	
221				820					825					830			
222	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe	Ile	Gln	Thr	Leu	Leu	
223			835					840					845				
224	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala	Val	Ile	Pro	Trp	Ile	
225		850					855					860					
226	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe	Ile	Phe	Leu	Arg	Arg	
227	865					870					875					880	
228	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg	Leu	Glu	Ser	Thr	Thr	
229					885					890					895		
230	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser	Leu	Gln	Gly	Leu	Trp	
231				900					905					910			
232	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys	Gln	Glu	Leu	Phe	Asp	
233			915					920					925				
234	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe	Leu	Phe	Leu	Thr	Thr	
235		930					935					940					
236	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile	Cys	Ala	Met	Phe	Val	
237	945					950					955					960	
238	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala	Lys	Thr	Leu	Asp	Ala	
239				965					970						975		
240	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu	Thr	Leu	Met	Gly	Met	
241				980					985					990			
242	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val	Glu	Asn	Met	Met	Ile	
243		995						1000					1005				
244	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu	Glu	Lys	Glu	Ala	Pro	
245		1010					1015					1020					
246	Trp	Glu	Tyr	Gln	Lys	Arg	Pro	Pro	Pro	Ala	Trp	Pro	His	Glu	Gly	Val	
247	1025					1030					1035					1040	
248	Ile	Ile	Phe	Asp	Asn	Val	Asn	Phe	Met	Tyr	Ser	Pro	Gly	Gly	Pro	Leu	
249					1045					1050						1055	
250	Val	Leu	Lys	His	Leu	Thr	Ala	Leu	Ile	Lys	Ser	Gln	Glu	Lys	Val	Gly	
251				1060					1065								

<210> 9  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sequence source:/note="synthetic construct"

<400> 9  
ctdgtgdgdcg tdgtdggn

18

*see item 9 on Ena Summary Sheet*

*FYI*

**Please Note:**

~~Use of n and/or Xaa have been detected in the Sequence Listing. Please review the~~  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/647,140

DATE: 06/18/2001

TIME: 16:26:36

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:1174 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9  
 L:1174 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9  
 L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
 L:1259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16  
 L:1259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16  
 L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
 L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
 L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
 L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
 L:1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
 L:1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
 L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

---